

GAP ALIGNMENT:
SEQ ID NO:3 to Spezyme Ethyl (New Matrix)

GAP of: NewB.pep check: 1170 from: 1 to: 514

WPDEF Seq ID Nos 3, translated by ThreeToOne
none

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad.
Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778
Length Weight: 2 Average Mismatch: -2.248

Quality: 2635 Length: 514
Ratio: 5.444 Gaps: 1
Percent Similarity: 98.967 Percent Identity: 98.967

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

NewB.pep x SPEZE.pep June 3, 2005 11:04 ..

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1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
51 SRSDVGYGVYDLYDLGEFNQKGAVRTKYGTTKAQYLQAIQAAHAAGMQVYA 100
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTTKAQYLQAIQAAHAAGMQVYA 100
101 DVVFDFHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 DVVFDFHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
151 YSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKAWDWEVDTENGNYDYL 200
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 YSSFKWRWYHFDGVDWDESRKLSRIYKFIIGKAWDWEVDTENGNYDYL 198
201 YADLDMHDPEVVTELKSWGKWVNTTNIDGFRLDIVKHIKFSSFPDWLS 250
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
199 YADLDMHDPEVVTELKNWGKWVNTTNIDGFRLDIVKHIKFSSFPDWLSY 248
251 VRSQTGKPLFTVGEYWSYDINKLHNHYIMKTNGTMSLFAPLHNKFYTAK 300

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GAP Alignment:
SEQ ID NO:3 to Spezyme Ethyl
(New Matrix)

||||| ||||| ||||| ||||| ||||| ||||| |||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLNKFYTAK 298

301 SGGTFDMRTLMTNTLMKDQPTLAFTFVDNHDTPEPGQALQSWVDPWFKPLA 350
||||| ||||| ||||| ||||| ||||| |||||
299 SGGAFDMRTLMTNTLMKDQPTLAFTFVDNHDTPEPGQALQSWVDPWFKPLA 348

351 YAFILTRQEYPCVFYGDYYGIPQYNIPSLKSKIDPILLIARRDYAYGTQH 400
||||| ||||| ||||| ||||| |||||
349 YAFILTRQEYPCVFYGDYYGIPQYNIPSLKSKIDPILLIARRDYAYGTQH 398

401 DYLDHSIDIIGWTREGVTEKPGSGLAALITDGPSSKWMYVGKQHAGKVFY 450
||||| |||||
399 DYLDHSIDIIGWTREGVTEKPGSGLAALITDGPSSKWMYVGKQHAGKVFY 448

451 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWPRKTTVSTIAWSITTRPWT 500
||||| |||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWPRKTT..... 484

EXHIBIT 9

GAP ALIGNMENT:
Sequence 3 (Figure 1) to Spezyme Ethyl (Old Matrix)

GAP of: NewA.pep check: 754 from: 1 to: 514

WPDEF A. Figure 1, sequence 3

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE

None

Symbol comparison table: oldpep.cmp CompCheck: 2543
 Dayhoff table (Schwartz, R. M. and Dayhoff, M. O. [1979] in Atlas of Protein Sequence and Structure, Dayhoff, M. O. Ed, pp. 353-358, National Biomedical Research Foundation, Washington D.C.) rescaled by dividing each value by the sum of its row and column, and normalizing to a mean of 0 and standard deviation of 1.0. The value for FY (Phe-Tyr) = RW = 1.425. Perfect matches are set to 1.5 and no matches on any row are . . .

Gap Weight: 30 Average Match: 5.402
Length Weight: 3 Average Mismatch: -3.964

Quality: 7203 Length: 514
Ratio: 14.882 Gaps: 1
Percent Similarity: 99.793 Percent Identity: 99.587

Match display thresholds for the alignment(s):

| = IDENTITY
: = 4
. = 1

NewA.pep x SPEZE.pep June 3, 2005 11:06 ..

1 aapfngtmmqyfewlpddgtlwtkvaneannlsslgitalwlppaykgt 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 AAPFNGTMMQYFEWLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50

51 srsvdvgvydlydlgefqnqkgtvrtkygtnaqylqaiqaahaagmqvya 100
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
51 SRSDVGVGVYDLYDLGEFNQKGTVRTKYGTTAQYLQAIQAHAAGMQVYA 100

101 dvvfdhkggadgtewvdavevnpsdrnqeisgytqiqawtkfdfpgrnt 150
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGYTQIQAUTKFDFPGRGNT 150

151 yssfkwrvyhfdfgvwdesrklsriykfrgigkawdwedtengnydym 200
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
151 YSSFKWRWYHFDFGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYM 198

201 yadldmdhpevvtelknwgkwyvnttnidgfrldavkhikfsffpdwlsy 250
||| ||| ||| ||| ||| ||| ||| |||
199 YADLDMDHPEVVTELKNWGKWVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248

GAP Alignment:
Sequence 3 (Figure 1) to Spezyme Ethyl
(Old Matrix)

251 vrsqtgkplftvgeywsydinklhnyitkttgtmslfadplhnkfytask 300
|||||||:|||||||:|||||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298

301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepgqalqswvdpwfkpla 350
|||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348

351 yafiltrqegypcvfygdyygipqynipslkskidplliarrdyaygtqh 400
|||||||
349 YAFILTRQEGYPFCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398

401 dyldhsdiigwtreggttekpgsglaalitdgpggskwmyvgkqhgkvfy 450
|||||||
399 DYLDHSIDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448

451 dltgnrsdtvtinsdgwgefkvnggsvvwprkttvstiarpittrpw 500
|||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWPRKTT..... 484

EXHIBIT 10

GAP ALIGNMENT:
Sequence 3 (Figure 1) to Spezyme Ethyl (New Matrix)

GAP of: NewA.pep check: 754 from: 1 to: 514

WPDEF A. Figure 1, sequence 3

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE

None

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad.
Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778
Length Weight: 2 Average Mismatch: -2.248

Quality: 2653 Length: 514
Ratio: 5.481 Gaps: 1
Percent Similarity: 99.587 Percent Identity: 99.587

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

NewA.pep x SPEZE.pep June 3, 2005 11:03 ..

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1 aapfngtmmqyfewylpddgtlwtkvaneannlssligitalwlppaykgt 50
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50

51 srsdvgygvydlydlgefqnqkgtvrtkygtaqylqaiqaahaagmqvya 100
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTAQYLQAIQAHAAGMQVYA 100

101 dvvfdhkggadgtewvdavevnpsdrnqeisgtyqiqawtkfdfpgrgnt 150
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150

151 yssfkwrwyhfdgvdwdesrklksriykfrrgikgawkadwevdtenynydylm 200
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
151 YSSFKWRWYHFDGVDWDESRKLKSRIYKF..IGKAWDWEVDTENGNYDYL 198

201 yadldmdhpevvteiknwgkwyvnttnidgfrldavkhikfsffpdwlsy 250
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | |
199 YADLDMDHPEVVTELKNWGKWyVNTTNIDGFRLDAVKHIFSFPPDWLSY 248

251 vrsqtgkplftvgeywsydinklhnyitktdgtmslfdaplnkfytask 300
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | |

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GAP Alignment:
Sequence 3 (Figure 1) to Spezyme Ethyl
(New Matrix)

249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDA PLHNKFYT ASK 298
301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepgqgalqswvd pwfkpla 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWF KPLA 348
351 yafiltrqegypcvfygdyygipqynipslkskidpliarrdyaygtqh 400
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
349 YA FILTRQEGYPCVFYGDYYGI PQYNIPSLKSKIDPLLIARRDYAYGTQH 398
401 dyldhsdiigwtreggtekpgsglaalitdgpggskwmyvgkqhagkvfy 450
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
399 DYLDHSDII GWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448
451 dltgnrsdtvtinsdgwgefkvnggsvswwprkttvstiarpitrpwt 500
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
449 DLTGNRSDTVTIN SDGWGEFKVNGGSVSWWPRKTT 484
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EXHIBIT 11

Alpha-Amylase Alignments

| | | |
|--------------------|--|----|
| Spezyme | AAPFNGTMMQ YFEWYLPDDG TLWTKVANEA NNLLSSLGIT A LWLPPAYKGT | 50 |
| SEQ ID NO:3 | AAPFNGTMMQ YFEWYLPDDG TLWTKVANEA NNLLSSLGIT A LWLPPAYKGT | 50 |
| Figure 1 | AAPFNGTMMQ YFEWYLPDDG TLWTKVANEA NNLLSSLGIT A LWLPPAYKGT | 50 |
| ATCC 31,195 | AAPFNGTMMQ YFEWYLPDDG TLWTKVANEA NNLLSSLGIT A LWLPPAYKGT | 50 |

| | | |
|--------------------|--|-----|
| Spezyme | SRSVDVGYG VY DLYDLGEFNQ KGTVRTKYGT KA QYLQAIQA AHAAGMQVYA | 100 |
| SEQ ID NO:3 | SRSVDVGYG VY DLYDLGEFNQ KGA VRTKYGT KA QYLQAIQA AHAAGMQVYA | 100 |
| Figure 1 | SRSVDVGYG VY DLYDLGEFNQ KGTVRTKYGT KA QYLQAIQA AHAAGMQVYA | 100 |
| ATCC 31,195 | SRSVDVGYG VY DLYDLGEFNQ KGTVRTKYGT KA QYLQAIQA AHAAGMQVYA | 100 |

| | | |
|--------------------|---|-----|
| Spezyme | DVVFDHKGG A DGTEWVDAVE VNPSDRNQE I SGTYQIQA WT KFDFPGRGNT | 150 |
| SEQ ID NO:3 | DVVFDHKGG A DGTEWVDAVE VNPSDRNQE I SGTYQIQA WT KFDFPGRGNT | 150 |
| Figure 1 | DVVFDHKGG A DGTEWVDAVE VNPSDRNQE I SGTYQIQA WT KFDFPGRGNT | 150 |
| ATCC 31,195 | DVVFDHKGG A DGTEWVDAVE VNPSDRNQE I SGTYQIQA WT KFDFPGRGNT | 150 |

| | | |
|--------------------|---|-----|
| Spezyme | YSSFKWRWYH FDGV DWDESR KLSRIYKF** I GKA DWEV D TENG NYD YLM | 198 |
| SEQ ID NO:3 | YSSFKWRWYH FDGV DWDESR KLSRIYKFRG I GKA DWEV D TENG NYD YLM | 200 |
| Figure 1 | YSSFKWRWYH FDGV DWDESR KLSRIYKFRG I GKA DWEV D TENG NYD YLM | 200 |
| ATCC 31,195 | YSSFKWRWYH FDGV DWDESR KLSRIYKFRG I GKA DWEV D TENG NYD YLM | 200 |

| | | |
|--------------------|---|-----|
| Spezyme | YADLDMDHPE VVTELKNWG K WYVNTTNIDG FRLDAVKHIK FSFFPDWLSY | 248 |
| SEQ ID NO:3 | YADLDMDHPE VVTELK SWG K WYVNTTNIDG FRLDAVKHIK FSFFPDWLS | 250 |
| Figure 1 | YADLDMDHPE VVTELKNWG K WYVNTTNIDG FRLDAVKHIK FSFFPDWLSY | 250 |
| ATCC 31,195 | YADLDMDHPE VVTELKNWG K WYVNTTNIDG FRLDAVKHIK FSFFPDWLSY | 250 |

| | | |
|--------------------|---|-----|
| Spezyme | VRSQTGKPLF TVGEYWSYDI NKLHNYITKT NGTMSLF DAP LHNKFYT ASK | 298 |
| SEQ ID NO:3 | VRSQTGKPLF TVGEYWSYDI NKLHNYIMKT NGTMSLF DAP LHNKFYT ASK | 300 |
| Figure 1 | VRSQTGKPLF TVGEYWSYDI NKLHNYITKT D GTMSLF DAP LHNKFYT ASK | 300 |
| ATCC 31,195 | VRSQTGKPLF TVGEYWSYDI NKLHNYITKT NGTMSLF DAP LHNKFYT ASK | 300 |

Alpha-Amylase Alignments
Page 2 of 2

| | | |
|--------------------|---|-----|
| Spezyme | SGGAFDMRTL MTNTLMKDQP TLAVTFVDNH DTEPGQALQS WVDPWFKPLA | 348 |
| SEQ ID NO:3 | SGGT F DMRTL MTNTLMKDQP TLAVTFVDNH DTEPGQALQS WVDPWFKPLA | 350 |
| Figure 1 | SGGAFDMRTL MTNTLMKDQP TLAVTFVDNH DTEPGQALQS WVDPWFKPLA | 350 |
| ATCC 31,195 | SGGAFDMRTL MTNTLMKDQP TLAVTFVDNH DTEPGQALQS WVDPWFKPLA | 350 |

| | | |
|--------------------|--|-----|
| Spezyme | YAFILTRQEG YPCVFYGDYY GIPQYNIPSL KSKIDPLLIA RRDYAYGTQH | 398 |
| SEQ ID NO:3 | YAFILTRQEG YPCVFYGDYY GIPQYNIPSL KSKIDPLLIA RRDYAYGTQH | 400 |
| Figure 1 | YAFILTRQEG YPCVFYGDYY GIPQYNIPSL KSKIDPLLIA RRDYAYGTQH | 400 |
| ATCC 31,195 | YAFILTRQEG YPCVFYGDYY GIPQYNIPSL KSKIDPLLIA RRDYAYGTQH | 400 |

| | | |
|--------------------|---|-----|
| Spezyme | DYLDHSIDIIG WTREGVTEKP GSGLAALITD GPGGSKWMYV GKQHAGKVFY | 448 |
| SEQ ID NO:3 | DYLDHSIDIIG WTREGVTEKP GSGLAALITD GPGGSKWMYV GKQHAGKVFY | 450 |
| Figure 1 | DYLDHSIDIIG WTREGG T TEKP GSGLAALITD GPGGSKWMYV GKQHAGKVFY | 450 |
| ATCC 31,195 | DYLDHSIDIIG WTREGVTEKP GSGLAALITD GPGGSKWMYV GKQHAGKVFY | 450 |

| | | |
|--------------------|--|-----|
| Spezyme | DLTGNRSDTV TINSDGWGEF KVNGGSVSvw VPRKTT | 484 |
| SEQ ID NO:3 | DLTGNRSDTV TINSDGWGEF KVNGGSVSvw VPRKTTVSTI AWSITTRPWT | 500 |
| Figure 1 | DLTGNRSDTV TINSDGWGEF KVNGGSVSvw VPRKTTVSTI ARPITTRPWT | 500 |
| ATCC 31,195 | DLTGNRSDTV TINSDGWGEF KVNGGSVSvw VPRKTTVST | 489 |

| | | |
|--------------------|-----------------|-----|
| Spezyme | | |
| SEQ ID NO:3 | DEFVRWTEPR LVAW | 514 |
| Figure 1 | GEFVRWTEPR LVAW | 514 |
| ATCC 31,195 | | |